

Figure No. 1

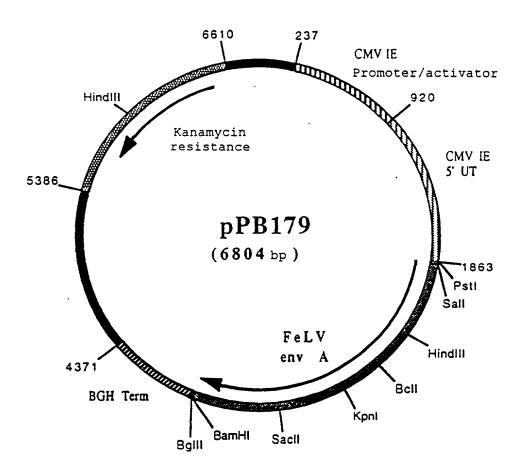


Figure No. 2

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  22 LeuValGlyValLeuLeuArgLeuAspValGlyMetAlaAsnProSerProHisGlnIleTyr
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- 190 GGAACCCTGACAGACGCCTTCCCTACCATGTATTTTGACTTATGTGATATAATAGGAAATACA 64 GlyThrLeuThrAspAlaPheProThrMetTyrPheAspLeuCysAspIleIleGlyAsnThr
- 253 TGGAACCCTTCAGATCAAGAACCATTCCCAGGGTATGGATGTGATCAGCCTATGAGGAGGTGG 85 TrpAsnProSerAspGlnGluProPheProGlyTyrGlyCysAspGlnProMetArgArgTrp
- 316 CGACAGAGAAACACACCCTTTTATGTCTGTCCAGGACATGCCAACCGGAAGCAATGTGGGGGG 106 ArgGlnArgAsnThrProPheTyrValCysProGlyHisAlaAsnArgLysGlnCysGlyGly
- 379 CCACAGGATGGGTTCTGCGCTGTATGGGGTTGCGAGACCACCGGGGAAACCTATTGGAGACCC 127 ProglnAspGlyPhacysAlaValTrpGlyCysGluThrThrGlyGluThrTyrTrpArgPro
- 442 ACCTCCTCATGGGACTACATCACAGTAAAAAAAGGGGTTACTCAGGGAATATATCAATGTAGT 148 ThrsersertrpAsptyrileThrvalLysLysGlyValThrGlnGlyIleTyrGlnCysSer
- 505 GGAGGTGGTTGGTGTGGGCCCTGTTACGATAAAGCTGTTCACTCCTCGACAACGGGAGCTAGT 169 GlyGlyGlyTrpcysglyProcystyrasplysalavalHisserserThrThrGlyAlaser :
- 568 GAAGGGGGCCGGTGCAACCCCTTGATCTTGCAATTTACCCAAAAGGGAAGACAAACATCTTGG 190 CluglyGlyArgCysAsnProLeuileLeuGlnPheThrGlnLysGlyArgGlnThrSerTrp
- 631 GATGGACCTAAGTCATGGGGGCTACGACTATACCGTTCAGGATATGACCCTATAGCCCTGTTC 211 AspGlyProlysserTrpGlyLeuArgLeuTyrArgserGlyTyrAspProlleAlaLeuPhe
- 694 TCGGTATCCCGGCAAGTAATGACCATTACGCCGCCTCAGGCCATGGGACCAAATCTAGTCCTG
  232 servalserArgGlnvalMetThrileThrProProGlnAlaMetGlyProAsnLeuValLeu
- 757 CCTGATCAAAAACCCCCATCCAGGCAATCTCAAATAGAGTCCCGAGTAACACCTCACCATTCC
- 253 ProAspGlnLysProProSerArgGlnSerGlnIleGluSerArgValThrProHisHisSer
- 820 CAAGGCAACGGAGGCACCCCAGGTGTAACTCTTGTTAATGCCTCCATTGCCCCTCTACGTACC 274 GlnglyAsnglyGlyThrProGlyValThrLeuValAsnAlaSerIleAlaProLeuArgThr
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- 1072 CCCTCCCCATCCTGCCTATCTACTCCGCAACATAAGCTAACTATATCTGAGGTGTCAGGGCAA 358 ProserProserCysLeuserThrProGlnHisLysLeuThrIleserGluValserGlyGln
- 1135 GGACTGTGCATAGGGACTGTTCCTAAGACCCACCAGGCTTTGTGCAATAAGACACAACAGGGA 379 GlyLeuCyslleGlyThrValProLysThrHisGlnAlaLeuCysAsnLysThrGlnGlnGly
- 1198 CATACAGGGGCTCACTATCTAGCCGCCCCCAATGGCACCTATTGGGCCTGTAACACTGGACTC 400 histhrGlyAlaHistyrLeuAlaAlaProAsnGlyThrTyrTrpAlaCysAsnThrGlyLeu

- 1261 ACCCCATGCATTTCCATGGCAGTGCTCAATTGGACCTCTGATTTTTGTGTCTTAATCGAATTA
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- 1324 TGGCCCAGAGTGACCTACCATCAACCCGAATACATTTACACACATTTCGACAAAGCTGTCAGG
  442 TrpProArgValThrTyrHisGlnProGluTyrIleTyrThrHisPheAspLysAlaValArg
- 1387 TTCCGAAGAGAACCAATATCACTAACCGTTGCCCTTATAATGGGAGGACTCACTGTAGGGGGC 463 PheArgArgGluProIleSerLeuthrValAlaLeuIleMetGlyGlyLeuthrValGlyGly
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- 1828 ATTATAGGCCCCTTACTAATCCTACTCCTAATTCTCCTCTTCGGCCCATGCATCCTTAACCGA 610 IleIleGlyProLeuLeulleLeuLeuleulleLeuLeuPheGlyProCysIleLeuAsnArg
- 1891 TTAGTGCAATTCGTAAAAGACAGAATATCTGTGGTACAAGCCTTAATTTTAACCCAACAGTAC 631 LeuvalginphevallysaspargileservalvalginalaLeuileLeuthrGinginTyr
- 1954 CAACAGATACAGCAATATGATCCGGACCGACCATGA
  652 GlnGlnIleGlnGlnTyrAspProAspArgPro...

Figure No. 3 (continuation and end)

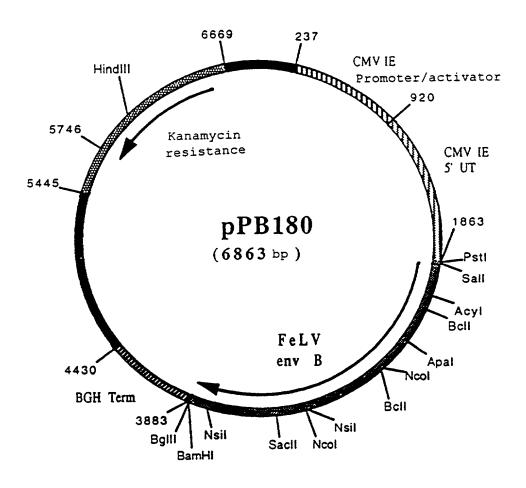


Figure No. 4

- 1 ATGTCTGGAGCCTCTAGTGGGACAGCCATTGGGGCTCATCTGTTTGGGGTCTCACCTGAATAC
- $\verb|| \verb|| \texttt{MetSerGlyAlaSerSerGlyThrAlaIleGlyAlaHisLeuPheGlyValSerProGluTyral}| \\$
- 64 AGGGTGTTGATCGGAGACGAGGGAGCCGGACCCTCAAGGTCTCTTTCTGAGGTTTCATTTTCG
- 22 ArgValLeuIleGlyAspGluGlyAlaGlyProSerArgSerLeuSerGluValSerPheSer
- 127 GTTTGGTACCAAAGACGCGCGCACGTCTTGTCATTTTTTGTCTGGTTGCGTCTTTTCTTGTC
  43 ValTrpTyrGlnArgArgAlaAlaArgLeuValIlePheCysLeuValAlaSerPheLeuVal
- 190 CCTTGTCTAACCTTTTTAATTGCAGAAACCGTCATGGGCCAAACTATAACTACCCCCTTAAGC 64 ProcysLeuthrPheLeuIleAlaGluthrValMetGlyGlnThrIleThrThrProLeuser
- 253 CTCACCCTTGATCACTGGTCTGAAGTCCGGGCACGAGCCCATAATCAAGGTGTCGAGGTCCGG
  85 LeuthrLeuAspHistrpSerGluValArgAlaArgAlaHisAsnGlnGlyValGluValArg
- 316 AAAAAGAATGGATTACCTTATGTGAGGCCGAATGGGTGATGAATGTGGGCTGGCCCCGA
- 196 LysLysLysTrpIleThrLeuCysGluAlaGluTrpValMetMetAsnValGlyTrpProArg
- 379 GAAGGAACTTTTTCTCTTGATAGCATTTCCCAGGTTGAAAAGAAGATCTTCGCCCCGGGACCA 127 GluGlyThrPheSerLeuAspSerIleSerGlnValGluLysLysIlePheAlaProGlyPro
- 442 TATGGACACCCCGACCAAGTTCCTTACATTACTACATGGAGATCCTTAGCCACAGACCCCCCT 148 TyrGlyHisProAspGlnValProTyrIleThrThrTrpArgSerLeuAlaThrAspProPro
- 169 SerTrpValArgProPheLeuProProProLysProProThrProLeuProGinProLeuSer
- 568 CCGCAGCCCTCCGCCCCTCTTACCTCTTCCCTCTACCCCGTTCTCCCCAAGCCAGACCCCCC 190 ProglnProserAlaProLeuThrserserLeuTyrProValLeuProLysProAspProPro
- 631 AAACCGCCTGTGTTACCGCCTGATCCTTCTCCCCTTTAATTGATCTCTTAACAGAAGAGCCA
- 211 LysProProValLeuProProAspProSerSerProLeuIleAspLeuLeuThrGluGluPro
- 694 CCTCCCTATCCGGGGGTCACGGGCCACCGCCATCAGGTCCTAGGACCCCAACCGCTTCCCCG
  232 ProprotyrProGlyGlyHisGlyProProProserGlyProArgThrProThrAlaserPro
- 253 IlealaserArgLeuArgGluArgArgGluAsnProAlaGluGluSerGlnAlaLeuProLeu
- 820 AGGGAAGGCCCCAACAACCGACCCCAGTATTGGCCATTCTCAGCTTCAGACTTGTATAACTGG
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- 295 LysSerHisAsnProProPheSerGlnAspProValAlaLeuThrAsnLeuIleGluSerIle
- 946 TTAGTGACGCATCAACCAACCTGGGACGACTGCCAGCAGCTCTTGCAGGCACTCCTGACAGGC
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- 2143 AGAAAGTACACAAAAACAGGAGATGGACACTTGGCTTAAAAACTTTCCCCAGGCGTGGGCAGA
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Figure No. 5 (continuation and end)

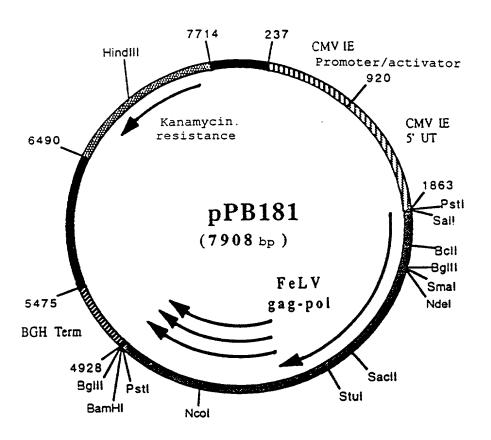


Figure No. 6

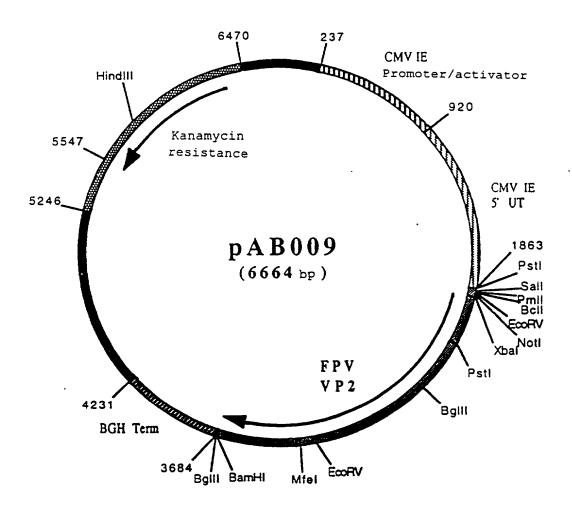


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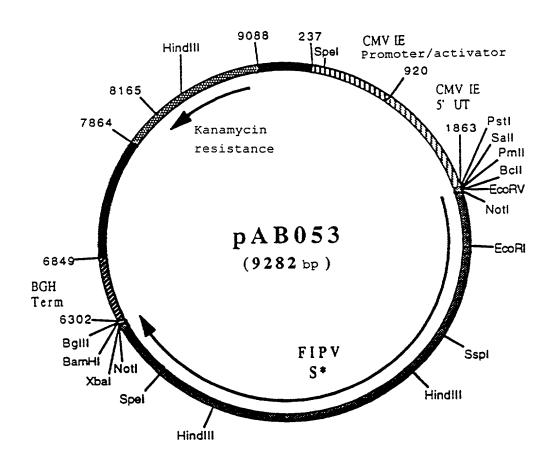


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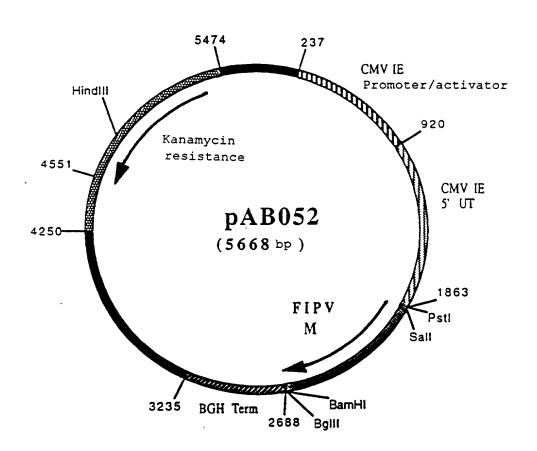


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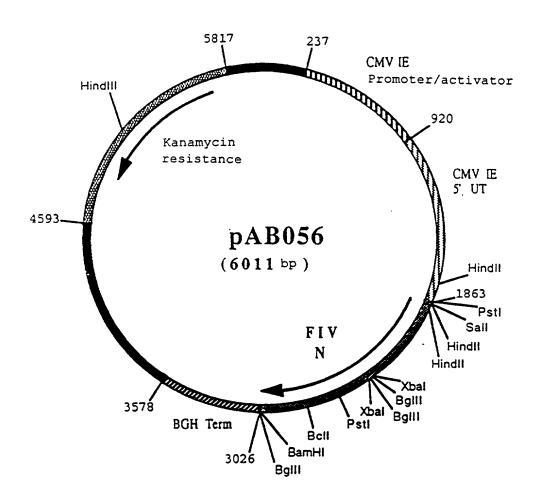


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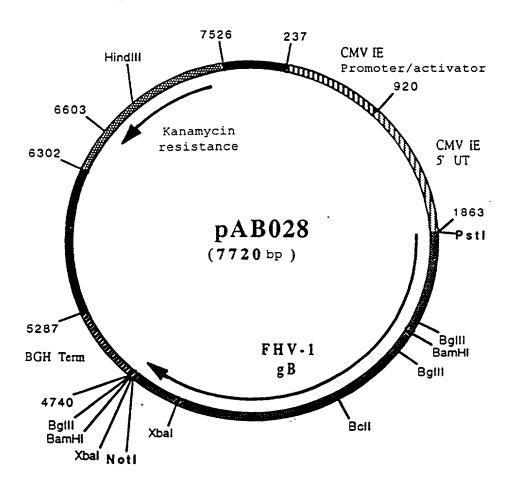


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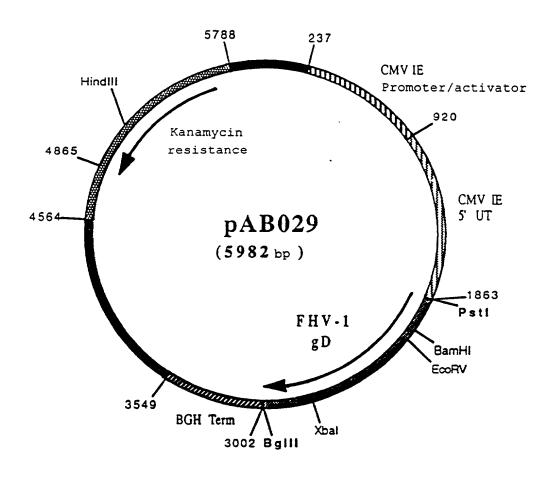


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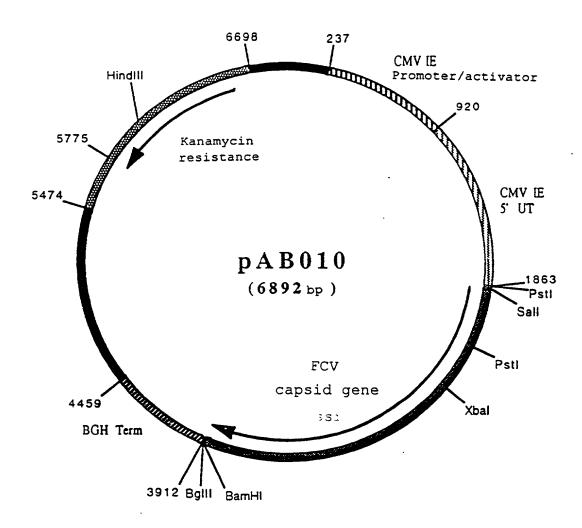


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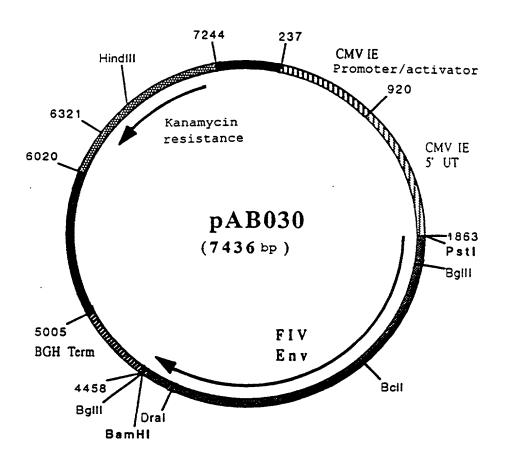


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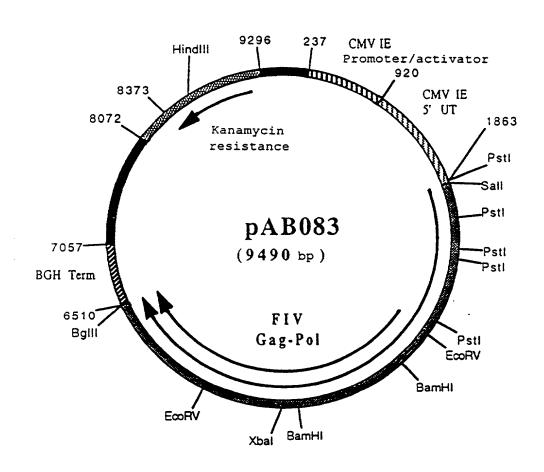


Figure No. 15

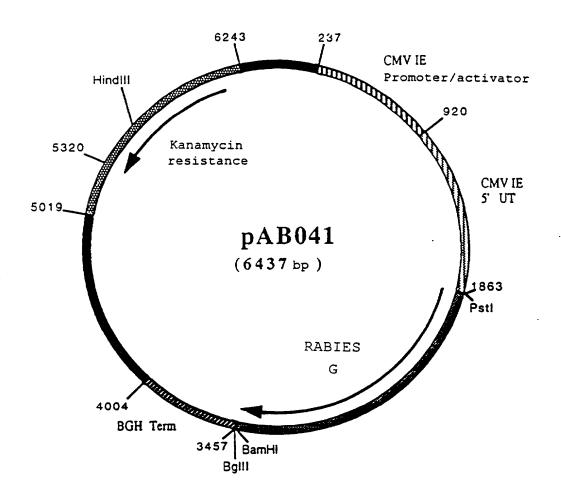


Figure No. 16